



SEQUENCE LISTING

COPY OF PAPERS
ORIGINALLY FILED

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<120> Methods of Controlling Gene Expression

<130> PB/5-31481A

<140> 09/896,186

<141> 2001-06-29

<160> 38

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Arabidopsis thaliana

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 85 90 95
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 145 150 155 160
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
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Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
  35             40             45

Thr Leu Thr Lys Pro Gln Glu Tyr Lys Ile Leu Val Asp Asn Ala
  50             55             60

Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
  65             70             75             80
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 Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
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      20              25              30

Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
      35              40              45

Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
      50              55              60

Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
      65              70              75              80

Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
      85              90              95

Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
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His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
      115              120              125

Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
      130              135              140

Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
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Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
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Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
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Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala
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35 40 45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
50 55 60

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
65 70 75 80

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
85 90 95

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
 100 105 110
 Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
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 130 135 140
 Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
 145 150 155 160
 Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
 165 170 175
 Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
 180 185 190
 Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
 195 200 205
 Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
 210 215 220
 Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
 225 230 235 240
 Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
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			20					25					30			
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Val	Cys	Cys	Lys	Leu	Gly	Val	Lys	Glu	Cys	Ile	Trp	Lys	Glu	Arg	Ser	
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Asn	Val	Lys	Glu	Arg	Ile	Trp	Lys	Glu	Ser	Ser	Asn	Val	Lys	Glu	His	
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          35             40             45

Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
          50             55             60

Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
          65             70             75             80

Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
          85             90             95

Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
          100             105             110

Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
          115             120             125

Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
          130             135             140

His Ile Arg His Tyr Leu His Pro Leu Leu Leu Ser Ser Ser Phe Glu
          145             150             155             160

Thr Ile Val Lys Val Tyr Leu Gly His Glu Gly Val Thr Lys Asp Lys
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Glu Leu Cys Met Ser Asn Trp Gly Ala Arg Ser Leu Ser His Asp Gln
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<213> C. elegans

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His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
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Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
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Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
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Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
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Arg	Asn	Leu	Glu	Ile	Leu	Asp	Asp	Thr	Val	Gln	Arg	Phe	Ala	Ile	Asn
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Lys	Glu	Glu	Glu	Ile	Leu	Leu	Ser	Asp	Met	Asn	Lys	Gln	Leu	Thr	Ser
				245					250					255	
Ile	Ser	Glu	Glu	Val	Met	Asp	Leu	Ala	Lys	His	Leu	Pro	His	Ala	Phe
				260				265					270		
Ser	Lys	Leu	Glu	Asn	Pro	Arg	Arg	Val	Ser	Ile	Leu	Leu	Lys	Asp	Ile
				275				280					285		
Ser	Glu	Asn	Leu	Tyr	Ser	Leu	Arg	Arg	Met	Ile	Ile	Gly	Ser	Thr	Asn
				290					295					300	
Ile	Glu	Thr	Glu	Leu	Arg	Pro	Ser	Asn	Asn	Leu	Asn	Leu	Leu	Ser	Phe
305					310					315					320
Glu	Asp	Ser	Thr	Thr	Gly	Gly	Val	Gln	Gln	Lys	Gln	Ile	Arg	Glu	His
				325					330					335	
Glu	Val	Leu	Ile	His	Val	Glu	Asp	Glu	Thr	Trp	Asp	Pro	Thr	Leu	Asp
				340				345					350		
His	Leu	Ala	Lys	His	Asp	Gly	Glu	Asp	Val	Leu	Gly	Asn	Lys	Val	Glu
				355				360					365		
Arg	Lys	Glu	Asp	Gly	Phe	Glu	Asp	Gly	Val	Glu	Asp	Asn	Lys	Leu	Lys
				370				375					380		
Glu	Asn	Met	Glu	Arg	Ala	Cys	Leu	Met	Ser	Leu	Asp	Ile	Thr	Glu	His
385					390					395					400
Glu	Leu	Gln	Ile	Leu	Glu	Gln	Gln	Ser	Gln	Glu	Glu	Tyr	Leu	Ser	Asp
				405					410					415	
Ile	Ala	Tyr	Lys	Ser	Thr	Glu	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn
				420				425					430		
Asp	Thr	Ser	Tyr	Val	Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met
				435				440					445		
Leu	Lys	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn	Asp	Thr	Ser	Tyr	Val
				450				455					460		
Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met	Leu	Lys	Ser	Leu	Glu
465					470					475					480
Asn	Leu	Asn	Ser	Gly	Thr	Val	Glu	Pro	Thr	His	Ser	Lys	Cys	Leu	Lys
				485					490					495	
Met	Glu	Arg	Asn	Leu	Gly	Leu	Pro	Thr	Lys	Glu	Glu	Glu	Glu	Asp	Asp

500					505					510					
Glu	Asn	Glu	Ala	Asn	Glu	Gly	Glu	Glu	Asp	Asp	Asp	Lys	Asp	Phe	Leu
	515						520					525			
Trp	Pro	Ala	Pro	Asn	Glu	Glu	Gln	Val	Thr	Cys	Leu	Lys	Met	Tyr	Phe
	530					535					540				
Gly	His	Ser	Ser	Phe	Lys	Pro	Val	Gln	Trp	Lys	Val	Ile	His	Ser	Val
545					550					555					560
Leu	Glu	Glu	Arg	Arg	Asp	Asn	Val	Ala	Val	Met	Ala	Thr	Gly	Tyr	Gly
				565					570						575
Lys	Ser	Leu	Cys	Phe	Gln	Tyr	Pro	Pro	Val	Tyr	Val	Gly	Lys	Ile	Gly
			580					585					590		
Leu	Val	Ile	Ser	Pro	Leu	Ile	Ser	Leu	Met	Glu	Asp	Gln	Val	Leu	Gln
		595					600					605			
Leu	Lys	Met	Ser	Asn	Ile	Pro	Ala	Cys	Phe	Leu	Gly	Ser	Ala	Gln	Ser
	610					615					620				
Glu	Asn	Val	Leu	Thr	Asp	Ile	Lys	Leu	Gly	Lys	Tyr	Arg	Ile	Val	Tyr
625					630					635					640
Val	Thr	Pro	Glu	Tyr	Cys	Ser	Gly	Asn	Met	Gly	Leu	Leu	Gln	Gln	Leu
				645					650					655	
Glu	Ala	Asp	Ile	Gly	Ile	Thr	Leu	Ile	Ala	Val	Asp	Glu	Ala	His	Cys
			660					665					670		
Ile	Ser	Glu	Trp	Gly	His	Asp	Phe	Arg	Asp	Ser	Phe	Arg	Lys	Leu	Gly
		675					680					685			
Ser	Leu	Lys	Thr	Ala	Leu	Pro	Met	Val	Pro	Ile	Val	Ala	Leu	Thr	Ala
	690					695					700				
Thr	Ala	Ser	Ser	Ser	Ile	Arg	Glu	Asp	Ile	Val	Arg	Cys	Leu	Asn	Leu
705					710					715					720
Arg	Asn	Pro	Gln	Ile	Thr	Cys	Thr	Gly	Phe	Asp	Arg	Pro	Asn	Leu	Tyr
				725					730					735	
Leu	Glu	Val	Arg	Arg	Lys	Thr	Gly	Asn	Ile	Leu	Gln	Asp	Leu	Gln	Pro
			740					745					750		
Phe	Leu	Val	Lys	Thr	Ser	Ser	His	Trp	Glu	Phe	Glu	Gly	Pro	Thr	Ile
		755					760					765			
Ile	Tyr	Cys	Pro	Ser	Arg	Lys	Met	Thr	Gln	Gln	Val	Thr	Gly	Glu	Leu
	770					775					780				
Arg	Lys	Leu	Asn	Leu	Ser	Cys	Gly	Thr	Tyr	His	Ala	Gly	Met	Ser	Phe
785					790					795					800
Ser	Thr	Arg	Lys	Asp	Ile	His	His	Arg	Phe	Val	Arg	Asp	Glu	Ile	Gln

				805				810				815			
Cys	Val	Ile	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asn	Lys	Ala	Asp
820								825				830			
Ile	Arg	Gln	Val	Ile	His	Tyr	Gly	Ala	Pro	Lys	Asp	Met	Glu	Ser	Tyr
835								840				845			
Tyr	Gln	Glu	Ile	Gly	Arg	Ala	Gly	Arg	Asp	Gly	Leu	Gln	Ser	Ser	Cys
850				855								860			
His	Val	Leu	Trp	Ala	Pro	Ala	Asp	Ile	Asn	Leu	Asn	Arg	His	Leu	Leu
865				870								875			
Thr	Glu	Ile	Arg	Asn	Glu	Lys	Phe	Arg	Leu	Tyr	Lys	Leu	Lys	Met	Met
				885				890				895			
Ala	Lys	Met	Glu	Lys	Tyr	Leu	His	Ser	Ser	Arg	Cys	Arg	Arg	Gln	Ile
				900				905				910			
Ile	Leu	Ser	His	Phe	Glu	Asp	Lys	Gln	Val	Gln	Lys	Ala	Ser	Leu	Gly
915								920				925			
Ile	Met	Gly	Thr	Glu	Lys	Cys	Cys	Asp	Asn	Cys	Arg	Ser	Arg	Leu	Asp
930				935								940			
His	Cys	Tyr	Ser	Met	Asp	Asp	Ser	Glu	Asp	Thr	Ser	Trp	Asp	Phe	Gly
945				950								955			
Pro	Gln	Ala	Phe	Lys	Leu	Leu	Ser	Ala	Val	Asp	Ile	Leu	Gly	Glu	Lys
				965				970				975			
Phe	Gly	Ile	Gly	Leu	Pro	Ile	Leu	Phe	Leu	Arg	Gly	Ser	Asn	Ser	Gln
				980				985				990			
Arg	Leu	Ala	Asp	Gln	Tyr	Arg	Arg	His	Ser	Leu	Phe	Gly	Thr	Gly	Lys
995				1000								1005			
Asp	Gln	Thr	Glu	Ser	Trp	Trp	Lys	Ala	Phe	Ser	Arg	Gln	Leu	Ile	Thr
1010				1015								1020			
Glu	Gly	Phe	Leu	Val	Glu	Val	Ser	Arg	Tyr	Asn	Lys	Phe	Met	Lys	Ile
1025				1030								1035			
Cys	Ala	Leu	Thr	Lys	Lys	Gly	Arg	Asn	Trp	Leu	His	Lys	Ala	Asn	Thr
				1045				1050				1055			
Glu	Ser	Gln	Ser	Leu	Ile	Leu	Gln	Ala	Asn	Glu	Glu	Leu	Cys	Pro	Lys
1060								1065				1070			
Lys	Phe	Leu	Leu	Pro	Ser	Ser	Lys	Thr	Val	Ser	Ser	Gly	Thr	Lys	Glu
1075								1080				1085			
His	Cys	Tyr	Asn	Gln	Val	Pro	Val	Glu	Leu	Ser	Thr	Glu	Lys	Lys	Ser
1090				1095								1100			
Asn	Leu	Glu	Lys	Leu	Tyr	Ser	Tyr	Lys	Pro	Cys	Asp	Lys	Ile	Ser	Ser

1105	1110	1115	1120
Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys	1125	1130	1135
Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr	1140	1145	1150
Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala	1155	1160	1165
Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu	1170	1175	1180
Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg	1185	1190	1195
Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu	1205	1210	1215
Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu	1220	1225	1230
Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala	1235	1240	1245
Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser	1250	1255	1260
Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg	1265	1270	1275
Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys	1285	1290	1295
Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val	1300	1305	1310
Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp	1315	1320	1325
Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp	1330	1335	1340
Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp	1345	1350	1355
Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro	1365	1370	1375
Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val	1380	1385	1390
Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro	1395	1400	1405
Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys			

1410

1415

1420

Thr Lys Arg Gly Gly Leu Phe Ser
 1425 1430

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 19
 cgacatgatc tgatacatcg ttatgccatt 30

<210> 20
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 20
 cattttataa taacgctgcg gacatctac 29

<210> 21
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

<400> 21
 atgtttgagt ttttcgcttc aggaggaagg tgcgccgacac aagaagctaa tgagccacca 60
 gttccgattt acattgtgac ggatccggtt caacttcctg ctgatttcct aaacccttct 120
 cctgaaaaga aattgggtat cggttttgac tgtgaggggtg ttgacctctg ccgacatggg 180
 aaactttgta tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240
 ggtggagagg tgattatgaa agcgtgtaag cctgcactcg agtctaatta catcacgaaa 300
 gttattcacg attgcaagcg tgacagttag gctctatact tccagtttgg gataagattg 360
 cacaatgttg tggacactca gattgcttat tctctgattg aagaacaaga agggcggagg 420
 agacctctag atgattacat atcgtttggt tcaactcctg ctgatccacg ttactgcggt 480
 atatccctatg aagagaaaga agaagttcga gttctcatgc gccaggaccc aaagttttgg 540
 acatacaggc ctatgactga gctcatgac cgcgagctg ctgatgatgt ccgcttcctt 600
 ctgtatctct atcacaaaat gatgggaaag ctaaatcagc ggtcactatg gcatcttgca 660
 gttcgtggtg ctttgtactg tcggtgtctc tgctgcatga atgatgctga ttttgctgat 720
 tggccaaccg ttctccaat tccagtttct ctcgttaagg tcgtatatgc tgtagagaca 780
 aagaaaaaaa gacgggtgac attagcttcg attgggttac tgattgtagt tggactttta 840
 aatgtggcag ataacctgaa gtcagaagat caatgtcttg aagaagagat cctgtcagtg 900
 cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960
 gccattaagg aagcttgcaa cgcggaatt ctaattggag gggcaaaggg tccacctgat 1020
 aaggttagtc ttattccata g 1041

<210> 22
<211> 346
<212> PRT
<213> Arabidopsis thaliana

<400> 22

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Asn	Glu	Pro	Pro	Val	Pro	Ile	Tyr	Ile	Val	Thr	Asp	Pro	Phe	Gln	Leu	
			20					25					30			
Pro	Ala	Asp	Phe	Leu	Asn	Pro	Ser	Pro	Glu	Lys	Lys	Leu	Val	Ile	Gly	
		35					40					45				
Phe	Asp	Cys	Glu	Gly	Val	Asp	Leu	Cys	Arg	His	Gly	Lys	Leu	Cys	Ile	
	50					55					60					
Met	Gln	Ile	Ala	Phe	Ser	Asn	Ala	Ile	Tyr	Leu	Val	Asp	Val	Ile	Glu	
	65				70				75						80	
Gly	Gly	Glu	Val	Ile	Met	Lys	Ala	Cys	Lys	Pro	Ala	Leu	Glu	Ser	Asn	
				85					90					95		
Tyr	Ile	Thr	Lys	Val	Ile	His	Asp	Cys	Lys	Arg	Asp	Ser	Glu	Ala	Leu	
			100					105					110			
Tyr	Phe	Gln	Phe	Gly	Ile	Arg	Leu	His	Asn	Val	Val	Asp	Thr	Gln	Ile	
		115					120					125				
Ala	Tyr	Ser	Leu	Ile	Glu	Glu	Gln	Glu	Gly	Arg	Arg	Arg	Pro	Leu	Asp	
		130				135					140					
Asp	Tyr	Ile	Ser	Phe	Val	Ser	Leu	Leu	Ala	Asp	Pro	Arg	Tyr	Cys	Gly	
	145				150					155					160	
Ile	Ser	Tyr	Glu	Glu	Lys	Glu	Glu	Val	Arg	Val	Leu	Met	Arg	Gln	Asp	
				165					170					175		
Pro	Lys	Phe	Trp	Thr	Tyr	Arg	Pro	Met	Thr	Glu	Leu	Met	Ile	Arg	Ala	
			180					185					190			
Ala	Ala	Asp	Asp	Val	Arg	Phe	Leu	Leu	Tyr	Leu	Tyr	His	Lys	Met	Met	
		195					200					205				
Gly	Lys	Leu	Asn	Gln	Arg	Ser	Leu	Trp	His	Leu	Ala	Val	Arg	Gly	Ala	
	210					215					220					
Leu	Tyr	Cys	Arg	Cys	Leu	Cys	Cys	Met	Asn	Asp	Ala	Asp	Phe	Ala	Asp	
	225				230					235					240	
Trp	Pro	Thr	Val	Pro	Pro	Ile	Pro	Val	Phe	Leu	Val	Lys	Val	Val	Tyr	
				245					250					255		
Ala	Val	Glu	Thr	Lys	Lys	Lys	Arg	Arg	Val	Thr	Leu	Ala	Ser	Ile	Gly	
			260					265					270			

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
 275 280 285

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
 290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
 305 310 315 320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
 325 330 335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
 340 345

<210> 23

<211> 1049

<212> DNA

<213> Arabidopsis thaliana

<400> 23

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atttctcccg	ttcttcttct	tcttcttcct	ctgctgctcc	gaccgtacaa	gctacaacct	180
ccgtccatgg	ccacgaggag	gatccaaatc	aaatcccca	taatatccgt	cgccaattgc	240
ctcgttccat	cacttcttct	acatcttata	aacgatttcc	tctctcccg	tgccgagcta	300
ggaattttcc	agcaatgagg	tttgggtgga	ggattttgta	tagcaagact	gctactgagg	360
ttgataagcg	agcaatgcag	cttattaaag	ttcttgatac	caagagagat	gaatctggaa	420
tagcttttgt	tggcttgga	attgagtga	gaccaagttt	tagaaaagg	gttctcccg	480
ggaagggtgc	gactgtccag	atatgtgtag	atagtaatta	ttgtgatgtt	atgcatattt	540
ttcattctgg	tatccctcaa	agtctccaac	atcttattga	agattcaaca	cttgtaaagg	600
taggtattgg	aattgatgg	gactctgtga	agcttttcca	tgactatgga	gttagtatca	660
aagatgttga	ggatctttca	gatttagcca	acaaaaaat	tggtggagat	aaaaaatggg	720
gccttgccct	actaactgag	acactgtgtt	gcaaagagct	cctgaagcca	aacagaatca	780
ggcttgggaa	ctgggagttt	tatcctctgt	caaagcagca	gttacaatac	gcagcaacgg	840
atgcttatgc	ttcatggcat	ctttacaagg	ttcttaagga	ccttcctgat	gctgtcagtg	900
gctcataacg	tgaaggagga	agcttaaagg	ttagcctata	acccaagag	ttagcatcaa	960
atgatatgat	acacctaata	tagtcaagta	gatgcaattc	ttgtgaatat	tgtatctagt	1020
tctggtccct	ttaaccgtcc	agaaactag				1049

<210> 24

<211> 288

<212> PRT

<213> Arabidopsis thaliana

<400> 24

Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
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Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
 20 25 30

Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
 35 40 45

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
 50 55 60
 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
 65 70 75 80
 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
 85 90 95
 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
 100 105 110
 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
 115 120 125
 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
 130 135 140
 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
 145 150 155 160
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
 165 170 175
 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
 180 185 190
 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
 195 200 205
 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
 210 215 220
 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
 225 230 235 240
 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
 245 250 255
 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
 260 265 270
 His Leu Tyr Lys Val Leu Lys Asp Leu Pro Asp Ala Val Ser Gly Ser
 275 280 285

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223>Description of Artificial Sequence: synthetic

<400> 25

ttcgaacca ccatcaaaca gg

<210> 26
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223>Description of Artificial Sequence: synthetic

 <400> 26
 ttgctgcaac tctctcaggg cc 22

<210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223>Description of Artificial Sequence: synthetic

 <400> 27
 tcagctgttg cccgtctcac t 21

<210> 28
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> Primer
 <222> 1...16
 <223> Description of Artificial Sequence: synthetic
 w=a or t; n=a, c, g, or t

 <400> 28
 wgtgnagwan canaga 16

<210> 29
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: synthetic

 <400> 29
 gctccgccca cataattcaa acaacac 27

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: synthetic

 <400> 30
 ttcgaaaaca ttacctccga tc 22

<210> 31

<211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: synthetic

<400> 31
 ggcttttgca ttggtatct actag 25

<210> 32
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: synthetic

<400> 32
 atgtcatcgt caaattggat cgacg 25

<210> 33
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: synthetic

<400> 33
 cgcttatcaa cctcagtagc agtcttg 27

<210> 34
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: synthetic

<400> 34
 ttatgagcca ctgacagcat cagg 24

<210> 35
 <211> 1749
 <212> DNA
 <213> Arabidopsis thaliana

<400> 35
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 AACACTGTGT GTTTACATGC GTTTTCAGAT TTAACCTATG TGTCTCCTGT TGTGTTCTTA 120
 TACCTACTCA AAGAATGCTA TAAACATGGT AGCTTGAAGG CAACAAAAAA GTTCCAAGCT 180
 TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAGGACC TGCTACTTTC 240
 ATTATTAAT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT 300
 TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA 360
 GATATTGTGT TGGCGAGAAA GCTAGCTGCT CAGTTCTTCC TTGCTACTGT TGGTGGATCT 420
 TTAACCTATG ATGAGAAGGT TATGGTGCAT ACTCTTAGAG TGTTTGATGT GAGGTAACT 480
 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGGA 540
 AATGCGTTTC TGAACAATA CATTTCTGAC TTGATCAAGT CGAAATCTTT CATGACGGCT 600
 GTGACTCTGT TAGAGCATTT CTCTTCCGT TTCCCTGGAG AAACCTTTCT TCAACAAATG 660
 GTTGAAGATA AAAATTTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGGCCAAGT 720

TTATGCATTC	TTGTTCAAGA	GTATGGCTCA	AGGAATATGC	TAAAGCAGGC	CTATAATATC	780
ATAAATAAGA	ACTATCTACA	GCATGACTTT	CCCGAATTGT	ATCACAAGTG	TAAAGAAAGT	840
GCTCTGAAGG	TTCTAGCAGA	AAAAGCATGT	TGGGATGTTG	CTGAAATTAA	GACAAAAGGT	900
GATAGACAGC	TTCTGAAGTA	TCTGGTATAC	TTGGCAGTGG	AAGCTGGATA	CTTGGAGAAG	960
GTTGATGAAC	TGTGCGATCG	ATATTCACCT	CAAGGGCTGC	CAAAAGCACG	AGAGGCTGAG	1020
GTTGCTTTTG	TTGAAAAAAG	CTTTCTGCGT	CTCAACGATC	TAGCTGTAGA	AGATGTAGTT	1080
TGGGTTGATG	AAGTCAACGA	GTTGAGAAAA	GCAACTTCTT	TTCTTGAAGG	ATGTAGAGTT	1140
GTGGGTATTG	ACTGTGAATG	GAAACCTAAT	TATATTAAAG	GCAGTAAACA	GAACAAGGTT	1200
TCAATCATGC	AAATTGGATC	TGATACCAAA	ATTTTCATAT	TGGACTTGAT	AAAGCTTTAC	1260
AATGACGCCT	CTGAAATTCT	GGACAACTGC	CTTAGTCACA	TTTTGCAATC	GAAGAGTACA	1320
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TACGACATGT	TGCTAGACAT	TCAAAATGTT	TTTAATGAAC	CATTTGGTGG	TTTAGCAGGA	1500
CTAACGAAGA	AAATATTGGG	AGTGTCTTTG	AACAAAACAA	GACGCAATAG	CGACTGGGAA	1560
CAAAGGCCTT	TGAGCCAGAA	TCAGCTTGAG	TATGCTGCTC	TTGATGCTGC	AGTGTTGATT	1620
CACATATTTT	GCCATGTTCG	CGATCATCCT	CCACATGACA	GTAGTTCAGA	GACAACCCAG	1680
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 Tyr Val Ser Pro Val Val Phe Leu Tyr Leu Leu Lys Glu Cys Tyr Lys
 35 40 45
 His Gly Ser Leu Lys Ala Thr Lys Lys Phe Gln Ala Leu Gln Tyr Gln
 50 55 60
 Val His Arg Val Leu Ala Asn Lys Pro Gln Pro Gly Pro Ala Thr Phe
 65 70 75 80
 Ile Ile Asn Cys Leu Thr Leu Leu Pro Leu Phe Gly Val Tyr Gly Glu
 85 90 95
 Gly Phe Ser His Leu Val Ile Ser Ala Leu Arg Arg Phe Phe Lys Thr
 100 105 110
 Val Ser Glu Pro Thr Ser Glu Glu Asp Ile Cys Leu Ala Arg Lys Leu
 115 120 125
 Ala Ala Gln Phe Phe Leu Ala Thr Val Gly Gly Ser Leu Thr Tyr Asp
 130 135 140
 Glu Lys Val Met Val His Thr Leu Arg Val Phe Asp Val Arg Leu Thr
 145 150 155 160
 Ser Ile Asp Glu Ala Leu Ser Ile Ser Glu Val Trp Gln Arg Tyr Gly
 165 170 175

Phe Ala Cys Gly Asn Ala Phe Leu Glu Gln Tyr Ile Ser Asp Leu Ile
180 185 190
Lys Ser Lys Ser Phe Met Thr Ala Val Thr Leu Leu Glu His Phe Ser
195 200 205
Phe Arg Phe Pro Gly Glu Thr Phe Leu Gln Gln Met Val Glu Asp Lys
210 215 220
Asn Phe Gln Ala Ala Glu Arg Trp Ala Thr Phe Met Gly Arg Pro Ser
225 230 235 240
Leu Cys Ile Leu Val Gln Glu Tyr Gly Ser Arg Asn Met Leu Lys Gln
245 250 255
Ala Tyr Asn Ile Ile Asn Lys Asn Tyr Leu Gln His Asp Phe Pro Glu
260 265 270
Leu Tyr His Lys Cys Lys Glu Ser Ala Leu Lys Val Leu Ala Glu Lys
275 280 285
Ala Cys Trp Asp Val Ala Glu Ile Lys Thr Lys Gly Asp Arg Gln Leu
290 295 300
Leu Lys Tyr Leu Val Tyr Leu Ala Val Glu Ala Gly Tyr Leu Glu Lys
305 310 315 320
Val Asp Glu Leu Cys Asp Arg Tyr Ser Leu Gln Gly Leu Pro Lys Ala
325 330 335
Arg Glu Ala Glu Val Ala Phe Val Glu Lys Ser Phe Leu Arg Leu Asn
340 345 350
Asp Leu Ala Val Glu Asp Val Val Trp Val Asp Glu Val Asn Glu Leu
355 360 365
Arg Lys Ala Thr Ser Phe Leu Glu Gly Cys Arg Val Val Gly Ile Asp
370 375 380
Cys Glu Trp Lys Pro Asn Tyr Ile Lys Gly Ser Lys Gln Asn Lys Val
385 390 395 400
Ser Ile Met Gln Ile Gly Ser Asp Thr Lys Ile Phe Ile Leu Asp Leu
405 410 415
Ile Lys Leu Tyr Asn Asp Ala Ser Glu Ile Leu Asp Asn Cys Leu Ser
420 425 430
His Ile Leu Gln Ser Lys Ser Thr Leu Lys Leu Val Ser Leu Thr Glu
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Asp Tyr Pro Asp His Lys Leu Ser Ser Gly Tyr Asn Phe Gln Cys Asp
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			20					25					30			
Leu	Asp	Ala	Glu	Trp	Lys	Pro	Gln	His	Ser	Asn	Thr	Ser	Ser	Phe	Pro	
		35					40					45				
Thr	Val	Thr	Leu	Leu	Gln	Val	Ala	Cys	Arg	Leu	Ser	His	Ala	Thr	Asp	
	50					55					60					
Val	Ser	Asp	Val	Phe	Leu	Ile	Asp	Leu	Ser	Ser	Ile	His	Leu	Pro	Ser	
65					70				75						80	
Val	Trp	Glu	Leu	Leu	Asn	Asp	Met	Phe	Val	Ser	Pro	Asp	Val	Leu	Lys	
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Leu	Gly	Phe	Arg	Phe	Lys	Gln	Asp	Leu	Val	Tyr	Leu	Ser	Ser	Thr	Phe	
			100					105						110		
Thr	Gln	His	Gly	Cys	Glu	Gly	Gly	Phe	Gln	Glu	Val	Lys	Gln	Tyr	Leu	
		115					120						125			
Asp	Ile	Thr	Ser	Ile	Tyr	Asn	Tyr	Leu	Gln	His	Lys	Arg	Phe	Gly	Arg	
	130					135					140					
Lys	Ala	Pro	Lys	Asp	Ile	Lys	Ser	Leu	Ala	Ala	Ile	Cys	Lys	Glu	Met	
145					150					155					160	
Leu	Asp	Ile	Ser	Leu	Ser	Lys	Glu	Leu	Gln	Cys	Ser	Asp	Trp	Ser	Tyr	
				165					170					175		
Arg	Pro	Leu	Thr	Glu	Glu	Gln	Lys	Leu	Tyr	Ala	Ala	Thr	Asp	Ala	His	
			180					185					190			
Cys	Leu	Leu	Gln	Ile	Phe	Asp	Val	Phe	Glu	Ala	His	Leu	Val	Glu	Gly	
		195					200					205				
Ile	Thr	Val	Gln	Asp	Leu	Arg	Val	Ile	Asn	Val	Gly	Leu	Gln	Glu	Ile	
	210					215					220					
Leu	Thr	Glu	Ser	Asp	Tyr	Ser	Ser	Lys	Ile	Val	Thr	Val	Lys	Leu	Cys	
225					230					235					240	
Lys	Ala	Thr	Asp	Val	Ile	Arg	Ser	Met	Ser	Glu	Asn	Gly	Gln	Asn	Ile	
				245					250					255		
Ala	Asn	Gly	Val	Val	Pro	Arg	Lys	Thr	Thr	Leu	Asn	Thr	Met	Pro	Met	
			260					265					270			
Asp	Glu	Asn	Leu	Leu	Lys	Ile	Val	Arg	Lys	Phe	Gly	Glu	Arg	Ile	Leu	
	275						280					285				
Leu	Lys	Glu	Ser	Asp	Leu	Leu	Pro	Lys	Lys	Leu	Lys	Lys	Lys	Thr	Arg	

290					295					300					
Arg	Arg	Val	Ala	Ser	Ser	Thr	Met	Asn	Thr	Asn	Lys	Gln	Leu	Val	Cys
305					310					315					320
Ser	Ala	Asp	Trp	Gln	Gly	Pro	Pro	Pro	Trp	Asp	Ser	Ser	Leu	Gly	Gly
				325					330					335	
Asp	Gly	Cys	Pro	Lys	Phe	Leu	Leu	Asp	Val	Met	Val	Glu	Gly	Leu	Ala
			340					345					350		
Lys	His	Leu	Arg	Cys	Val	Gly	Ile	Asp	Ala	Ala	Ile	Pro	His	Ser	Lys
		355					360					365			
Lys	Pro	Asp	Ser	Arg	Glu	Leu	Leu	Asp	Gln	Ala	Phe	Lys	Glu	Asn	Arg
	370					375					380				
Val	Leu	Leu	Thr	Arg	Asp	Thr	Lys	Leu	Leu	Arg	His	Gln	Asp	Leu	Ala
385					390					395					400
Lys	His	Gln	Ile	Tyr	Arg	Val	Lys	Ser	Leu	Leu	Lys	Asn	Glu	Gln	Leu
				405					410					415	
Leu	Glu	Val	Ile	Glu	Thr	Phe	Gln	Leu	Lys	Ile	Ser	Gly	Asn	Gln	Leu
			420					425					430		
Met	Ser	Arg	Cys	Thr	Lys	Cys	Asn	Gly	Lys	Phe	Ile	Gln	Lys	Pro	Leu
		435					440					445			
Ser	Ile	Glu	Glu	Ala	Ile	Glu	Ala	Ala	Lys	Gly	Phe	Gln	Arg	Ile	Pro
	450					455					460				
Asn	Cys	Leu	Phe	Asn	Lys	Asn	Leu	Glu	Phe	Trp	Gln	Cys	Met	Asn	Cys
465					470					475					480
His	Gln	Leu	Tyr	Trp	Glu	Gly	Thr	Gln	Tyr	His	Asn	Ala	Val	Gln	Lys
				485					490					495	
Phe	Met	Glu	Val	Cys	Lys	Leu	Ser	Glu							
			500					505							